**Claims**

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

a) a nucleic acid sequence, selected from the group Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247,

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 2-4, 6-10, 12-14, 16-19, 21, 23, 24, 26-33, 35-37, 39, 41-44, 46, 47, 49, 51-55, 58-64 and 217-247, characterized in that it is expressed elevated in normal prostate tissue.

4. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for use as a vehicle for gene transfer.

5. A nucleic acid sequence according to ~~claims 1 to 4~~ Claim 3, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to ~~claims 1 to 4~~ Claim 3, wherein it has 95% homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in ~~claims 1 to 6~~ Claim 3, in such a sufficient amount that they hybridize with the sequences according to ~~claims 1 to 6~~ Claim 3.

8. A nucleic acid sequence according to ~~claims 1 to 7~~ Claim 3, wherein the size of the fragment has a length of at least 50 to 2500 bp.

9. A nucleic acid sequence according to ~~claims 1 to 7~~ Claim 3, wherein the size of the fragment has a length of at least 150 to 2000 bp.

10. A nucleic acid sequence according to one of ~~claims 1 to 9~~ Claim 3, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to ~~one of claims 1 to 9~~ Claim 3, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to ~~one of claims 11 and 12~~ Claim 11, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to ~~claims 1 to~~ Claim 3 for producing full-length genes.

15. A DNA fragment, comprising a gene that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to ~~one of claims 1 to 10~~ Claim 3.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to ~~one of claims 16 or 17~~ Claim 16, wherein the prokaryotic cell system is E. coli and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to ~~claims 16 to 18~~ Claim 16 are cultivated.

20. An antibody which is directed against a polypeptide or a fragment which by the nucleic acids of sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. A protein according to claim 20, wherein it originates from a phage display.

23. Polypeptide partial sequences according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114,

116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

24. Polypeptide partial sequences according to claim 22, with at least 80% homology to these sequences.

25. Polypeptide partial sequences according to claim 22, with at least 90% homology to these sequences.

A 26. Use of polypeptide partial sequences of Claim 23 according to sequences Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as tools for finding active agents against prostate cancer.

A 27. Use of nucleic acid sequences of Claim 2 according to sequences Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 for expression of polypeptides that can be used as tools for finding active agents against prostate cancer.

A 28. Use of nucleic acid sequences of Claim 2 Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247 in sense or antisense form.

A 29. Use of polypeptide partial sequences of Claim 23 Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295 as pharmaceutical agents in gene therapy for treatment of prostate cancer.

A 30. Use of polypeptide partial sequences of Claim 23 Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq.

ID No. 248-295 to produce a pharmaceutical agent for treatment of prostate cancer.

31. Pharmaceutical agent, containing at least one polypeptide partial sequence of Claim 23, Seq. ID No. 66-71, 73-75, 82, 83, 90-93, 97-105, 109, 111-114, 116-124, 128-137, 139-149, 152, 154-165, 168-173, 183-195, 214-216 and up to Seq. ID No. 248-295.

32. A nucleic acid sequence according to ~~claims 1 to 10~~ Claim 3, wherein it is a genomic sequence.

33. A nucleic acid sequence according to ~~claims 1 to 10~~ Claim 3, wherein it is an mRNA sequence.

34. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, obtainable from cDNAs of sequences of Claim 2, Seq. ID No. 3, 4, 6-8, 12, 16-19, 21, 23, 24, 26-33, 35, 37, 41-44, 46, 47, 49, 51, 53, 54, 58-64 and 217-247.

35. Use of the genomic genes according to ~~claim~~ 33, together with suitable regulatory elements.

36. Use according to claim 34, wherein the regulatory element is a suitable promoter and/or enhancer.

37. A nucleic acid sequence according to ~~claims 1 to 7~~ Claim 3, wherein the size of the fragment has a length of at least 400 to 1900 bp.